

1  
A

2 32  
 CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG  
 arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr

62 92  
 TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC  
 ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser

122 152  
 TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA  
 trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala

182 212  
 GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA  
 glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272  
 AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG  
 ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332  
 GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG  
 ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp

362 392  
 TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT  
 phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

Cadherin  
 422 |xxx cleavage xx| 452  
 GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC  
 glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512  
 AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA  
 ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572  
 CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT  
 leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632  
 GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG  
 val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro

662 692  
 AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG  
 asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752  
 CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT  
 his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro

782 812  
 TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG  
 ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842 872  
 ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT  
 ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

FIG. 1 (1 of 5)

Cadherin  
|xx EC motif xx|

932	GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT
	val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his
962	
992	AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
	lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr
1022	
1052	TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
	ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile
1082	
1112	ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
	met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro
1142	
1172	ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
	ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val
1202	
1232	GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
	ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu
1262	
1292	ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
	thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu
1322	
1352	ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
	ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr
1382	
1412	GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
	asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys
1442	
1472	TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
	phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser
1502	
1532	AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
	lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu
1562	
1592	ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
	met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser
1622	
1652	CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
	gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu
1682	
1712	GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
	asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu
1742	
1772	GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
	ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu
1802	
1832	TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
	ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

FIG. 1 (2 of 5)

1862  
 CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT  
 gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1892  
 GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT  
 ala thr gln arg ala leu val ser lys phe

1922  
 CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC  
 pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1952  
 CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC  
 gln cys ala asp leu cys leu arg leu leu

1982  
 CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA  
 arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2012  
 CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA  
 arg ser his pro ser ala ser leu tyr leu

2042  
 CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA  
 leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2072  
 AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA  
 asn phe ala arg val lys met gln val pro

2102  
 ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT  
 met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2132  
 CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT  
 gln asn phe asn glu glu phe leu arg arg

2162  
 TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT  
 ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2192  
 GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT  
 glu asp leu glu leu arg glu thr thr phe

2222  
 CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA  
 pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2252  
 CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA  
 leu his met ile leu ser asp thr val lys

2282  
 ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag  
 met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2312  
 TTG ATT GAT CTA ATG tac aga att gcc aag  
 leu ile asp leu met tyr arg ile ala lys

2342  
 ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC  
 gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2372  
 ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC  
 thr trp leu gln asn met ala gly lys his

2402  
 TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT  
 ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

|xxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxxxxxxxxxxxx|

2492  
 GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT  
 ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522  
 CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA  
 gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2552  
 TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA  
 ser ala val ser asp asp val val ser pro

2582  
 GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG  
 asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2612  
 TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG  
 phe thr glu ser gly leu val gly leu leu

2642  
 GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC  
 glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2672  
 GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC  
 gly met tyr glu ala val asn glu val tyr

|xxx ITAM xxx|

2732  
 AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT  
 lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762  
 GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG  
 gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2792  
 GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG  
 val his gln ser thr gly trp glu arg met

FIG. 1 (3 of 5)

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2822      |xxxxxx ITAM xxxx|      2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882      2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942      2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002      3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062      3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122      3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182      3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242      3272      |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil -1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|      3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422      3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482      3512      |xxxxxxxxxxxxx
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602      3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro STP

3662      3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722      3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782      3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

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FIG. 1 (4 of 5)

3842	3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA	GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG
3902	3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT	CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA
3962	3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA	GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT
4022	4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT	AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG
4082	4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA	TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC
4142	
CTC	

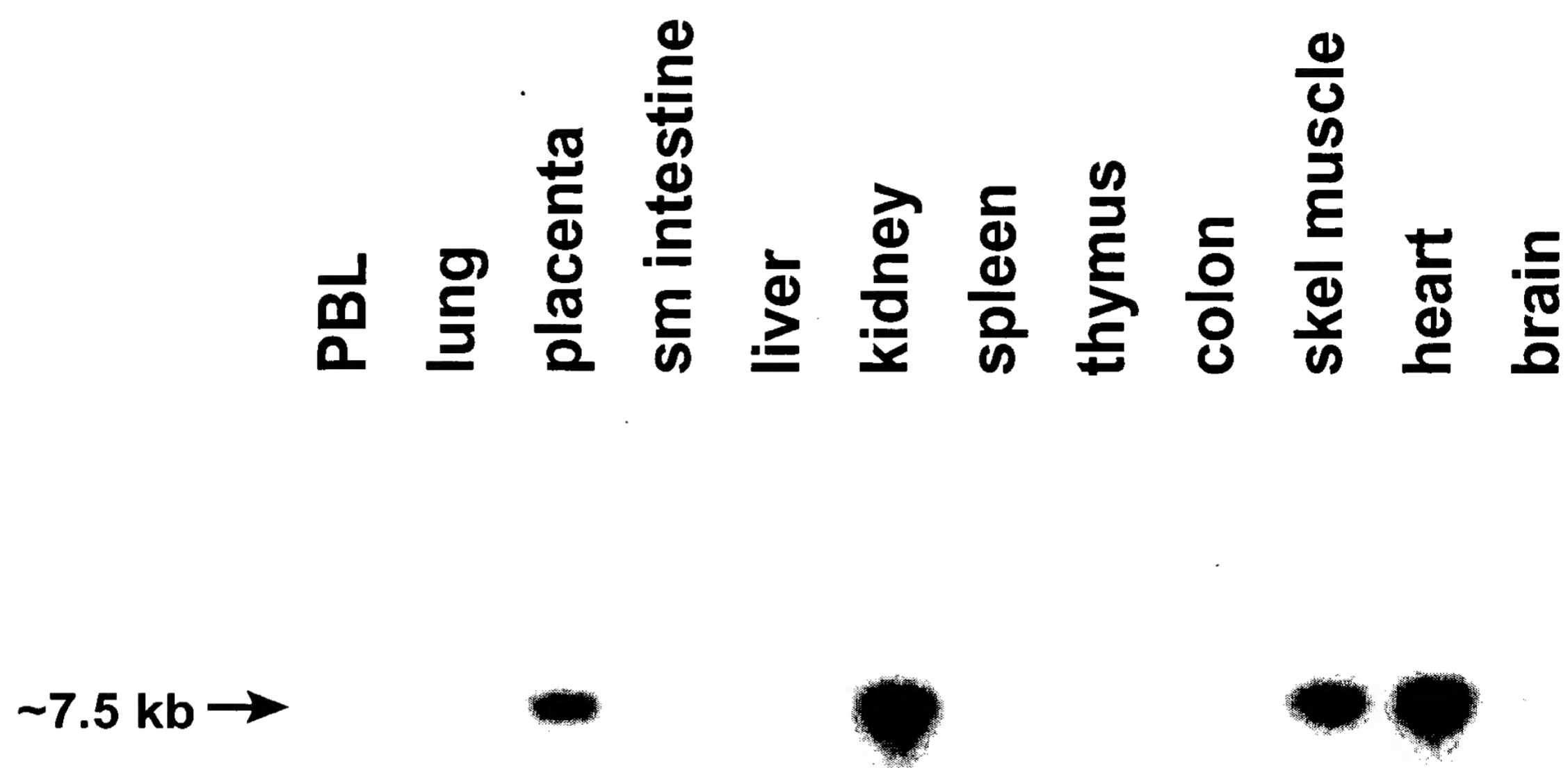


FIG. 2A

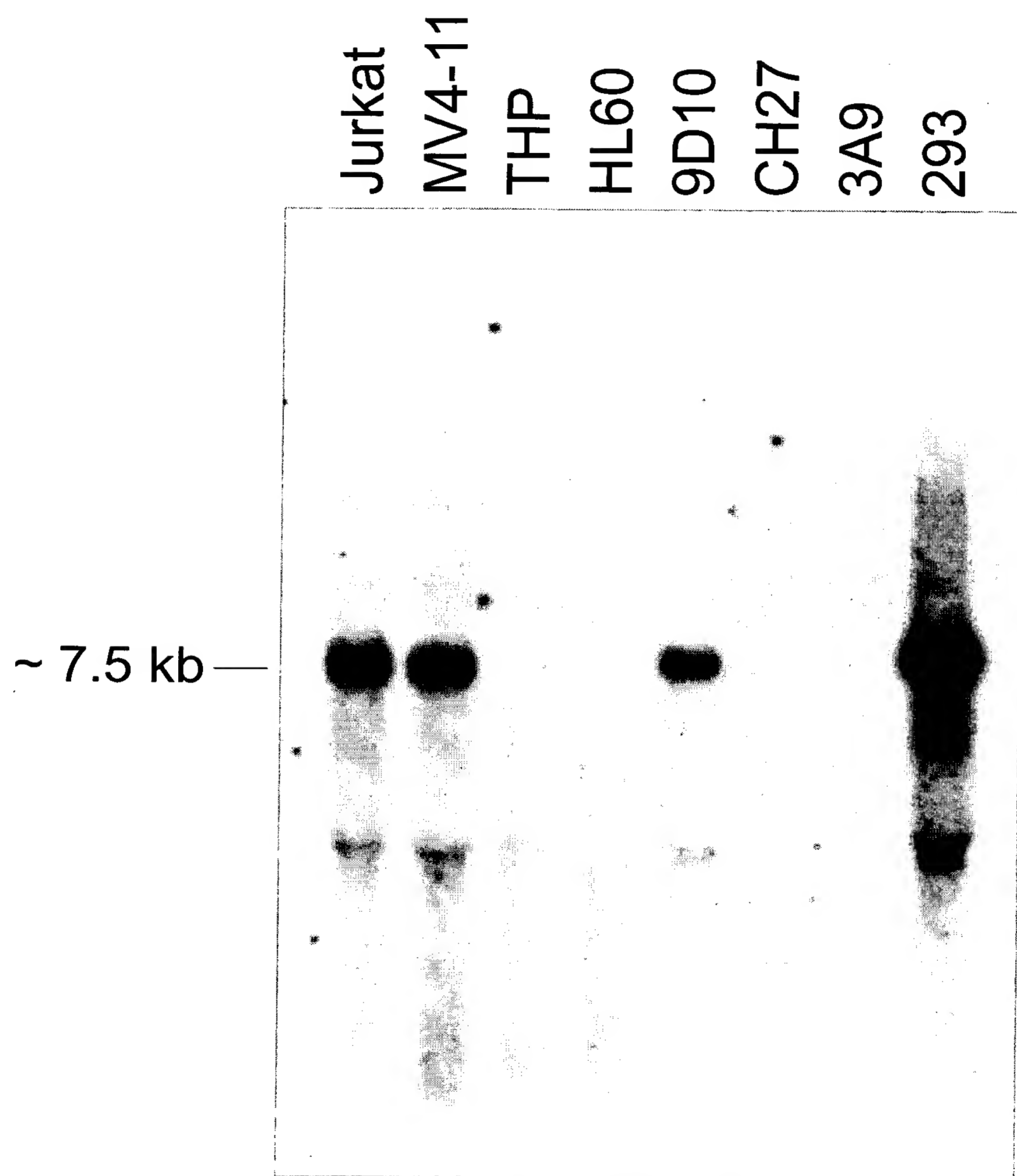


FIG. 2B

HC2A	-----
KIAA	ASGNLDKNARFS AIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSPSPSAES
HC5	-----
HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5	-----

FIG. 3A (1 of 5)

	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIKSMAQHLEIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMAQHLEIENSKVKLLRNQRFPPASYHHAVETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMAQHLEIDTNKIQLPRPQRFPPESYQNELDNLMVLSDHVIWKYKD
HC3	SALQQAWFFFEELMVKSMVHHLYFNDKLEAPRKSRRPFRFMDDDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLKQYKFDL
HC3	DTEMVERLNTSLAFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVQCQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHEHYVTNLNLPSSLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
	Cadherin EC motif
HC2A	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNNQAKIAQ
HC1	CRKHFLIGILLREVGFALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGLVLTTELAVILDPDAEGLFGLHKKVINMVHNLSSHDSDPRYSQPQIKARVAM
HC5	SSTS-SPGLLTTELAAALDAEGEGISEVQRKAIVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPPFVGLLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYKDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFDPQGNLTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI PRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

FIG. 3A (2 of 5)

HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRSQVM
HC1	QNFRLGKRNIIRKIAAAF--KFVQSTQNNGTCLKGSNPSCQTSGLLAQWMHSTSRHEGKH
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM

HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK--NALSNNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPMLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLOHCFATQALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLRALIA

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGGKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGGKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGGKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCEVLKCCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK
HC5	KFGDLLFEEVEEQCFDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK

HC2A	LQVIISVSQLIADVVGIGETRFFQQSLSIINNCANSRDLIKHTSFSSDVKDCLKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRFFQQSLSIINNCANSRDLIKHTSFSSDVKDCLKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRFFQQSLSIINNCANSRDLIKHTSFSSDVKDCLKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRDPMLARAFPAEVKDCLKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDCLKRIRTVLM
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPTQVEELLCNLNSILY

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAKGHSERSNHAEEAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPLRLTLWLQNMAEKHTKKKCYTEAAMCLVHA

		SH3	
HC2A	TALVAEYLTRKGV-----		-----FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----		-----VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYLTRKEAD-----		-----LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFLHRKKL-----		-----FPNGCSAFKKITPN
HC1	AALIAEYLKRKGWYKVEKIOTASLLSEDTHPCDNSLLTTFSGGSMFSGMGWPAFLSITPN		
HC3	AALVAEYLSMLED-----		-----RKYLPVGCVTFFQNISN
HC5	AALVAEYLSMLED-----		-----HSYLPVGSVSFQNISN

FIG. 3A (3 of 5)

HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM

HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADI FHQALLEGNTATEVS
HC1	QHRSQLPIIRGK--NALSNPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMAKKNVFTALRS LIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCS SIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5	KFGDLLFEEVEQC FDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK

HC2A	LQVIISVSQLIADVVGIGETRFOQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRFOQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRFOQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFI INNFANS DR PMLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKN GDFSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTWLQNMAGKHSERSNHA EAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQAS PDLRLTWLQNMAEKHTKKKCYTEAMCLVHA

		SH3	
HC2A	TALVAEYI	TRKGV-----	-----FRQGCTAFRVITPN
KIAA	TALVAEYI	TRKEA-----	-----VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYI	TRKEAD-----	-----LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEYI	HRKKL-----	-----FPNGCSAFKKITPN
HC1	AALIAEYI	KRKGYWKVEKIC	TASLLSEDT HPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3	AALVAEYI	SMLED-----	-----RKYLPVGCVT FQNISSN
HC5	AALVAEYI	SMLED-----	-----HSYLPVGSVS FQNISSN

FIG. 3A (3 of 5)

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPEPHVGTCTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 3A (5 of 5)

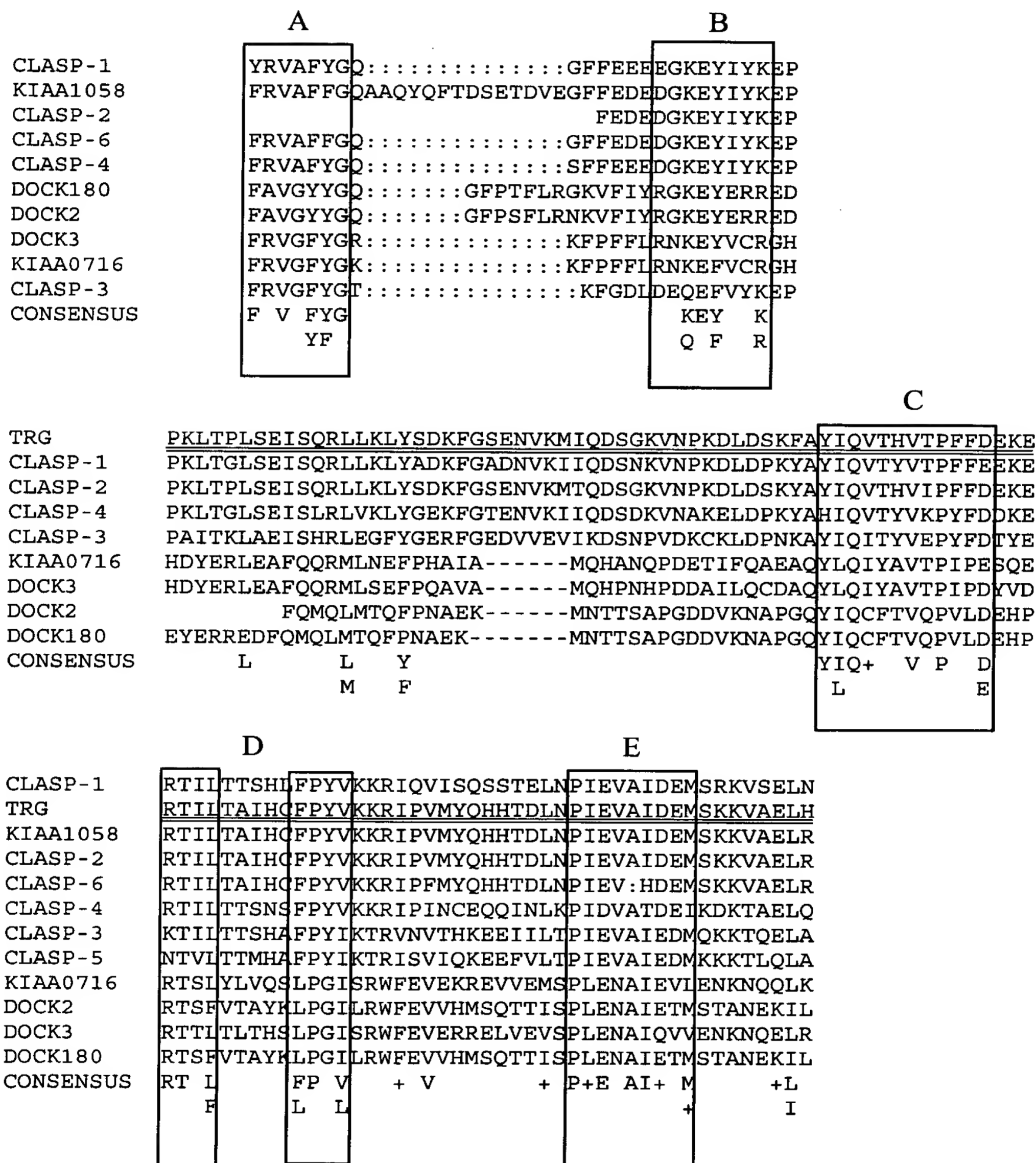


FIG. 3B (1 of 2)

	F										G									
CLASP-1	SLQLKLOGSVSVKVNAGPMAYARAFLEETNAKKYEDNQV--KLLKEIFRQFADACGQALD										KLLKEVFRQFVEACGQALA									
TRG	KLQLKLOGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA										KLLKEVFRQFVEACGQALA									
KIAA1058	KLQLKLOGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA										KLLKEVFRQFVEACGQALA									
CLASP-2	KLQLKLOGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA										KLLKEVFRQFVEACGQALA									
CLASP-6	KLQLKLOGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA										KLLKEVFRQFVEACGQALA									
CLASP-3	MLQMLQGSVGTTVNQGPLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR										KLLKEVFRQFVEACGQALA									
CLASP-4	QLQLKLOGCVSVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFI--QACSI										KLLKEVFRQFVEACGQALA									
CLASP-5	MLQMLQGSVGATVNTQGPLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE										KLLKEVFRQFVEACGQALA									
KIAA0716	ELTMCLNGVIDAAVNGGVSRVYQEAFFVKEYILSHPEEDGEKIARLRELMLEQAQILEFGLA										KLLKEVFRQFVEACGQALA									
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFFTTEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK										KLLKEVFRQFVEACGQALA									
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAFFDKDYINKHFGDAEKITQLKELMQEQVHVLGVGLA										KLLKEVFRQFVEACGQALA									
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFFTTEYVRDHPFAHEKIEKLKDLIAWQIPFLAEGIR										KLLKEVFRQFVEACGQALA									
CONSENSUS	L	M	L+G	V	VN	G	Y	AFL	+	+	E							L+		L
				I			V	V	F	+										I

DOCK2=KIAA0209  
DOCK3=KIAA0299  
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

2 32  
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG

62 92  
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC

122 152  
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA

182 212  
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA  
met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272  
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG  
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332  
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG  
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp  
ref 1.1 and 1.2  
ref 2.1 and 2.2 ↓

362 392  
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT  
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

422 452  
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC  
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512  
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA  
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572  
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT  
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632  
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG  
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro  
ref 3.1 and 3.2 ↓

662 692  
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG  
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752  
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT  
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro  
ref 4.1 and 4.2 ↓

782 815  
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG  
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842 872  
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT  
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

FIG. 4A (1 of 14)

902	GTG TTA ACA GAG CTG GCT GTC ATT TTA gac	932	cct gat gct gaa gga ctg TTT GGA TTG CAT
	val leu thr glu leu ala val ile leu asp		pro asp ala glu gly leu phe gly leu his
962	AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA	992	CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
	lys lys val ile asn met val his asn leu		leu ser ser his asp ser asp pro arg tyr
1022	TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC	1052	ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
	ser asp pro gln ile lys ala arg val ala		met leu tyr leu pro leu ile gly ile ile
1082	ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT	1112	ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
	met glu thr val pro gln leu tyr asp phe		thr glu thr his asn gln arg gly arg pro
1142	ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT	1172	GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
	ile cys ile ala thr asp asp tyr glu ser		glu ser gly ser met ile ser gln thr val
1202	GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT	1232	CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
	ala met ala ile ala gly thr ser val pro		gln leu thr arg pro gly ser phe leu leu
	↓		ref5.1 and 5.2
1262	ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC	1292	TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
	thr ser thr ser gly arg gln his thr thr		phe ser ala glu ser ser arg ser leu leu
1322	ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA	1352	GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
	ile cys leu leu trp val leu lys asn ala		asp glu thr val leu gln lys trp phe thr
1382	GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA	1412	TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
	asp leu ser val leu gln leu asn arg leu		leu asp leu leu tyr leu cys val ser cys
1442	TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA	1472	CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
	phe glu tyr lys gly lys lys val phe glu		arg met asn ser leu thr phe lys lys ser
1502	AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT	1532	ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
	lys asp met arg ala lys leu glu glu ala		ile leu gly ser ile gly ala arg gln glu
	↓		ref 6.1 and 6.2
1562	ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG	1592	AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
	met val arg arg ser arg gly gln leu glu		arg ser pro ser gly ser ala phe gly ser
1622	CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG	1652	ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
	gln glu asn leu arg trp arg lys asp met		thr his trp arg gln asn thr glu lys leu
1682	GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA	1712	GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
	asp lys ser arg ala glu ile glu his glu		ala leu ile asp gly asn leu ala thr glu

FIG. 4A (2 of 14)

1742	1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA	ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu
1802	1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC	ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn
1862	1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT	gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe
1922	1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC	pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu
1982	2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA	arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu
2042	2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA	leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro
2102	2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT	met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg
2162	2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT	ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe
2222	2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA	pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys
2282	2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag	met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys
2342	2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC	gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his
2402	2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT	ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val
2462	2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT	ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe
↓ ref 8.1 and 8.2	
2525	2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA	gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro
2582	2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG	asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

FIG. 4A (3 of 14)

2642	2672
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT	GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
glu gln ala ala ala ser phe ser met ala	gly met tyr glu ala val asn glu val tyr
2702	2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT	CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
lys val leu ile pro ile his glu ala asn	arg asp ala lys lys leu ser thr ile his
	ref 9.1
2762	2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT	GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
gly lys leu gln glu ala phe ser lys ile	val his gln ser thr gly trp glu arg met
2822	2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT	GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr	gly thr lys phe gly asp leu asp glu gln
2882	2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC	AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr	lys leu ala glu ile ser his arg leu glu
ref 10.1 and 10.2	
2945	2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT	GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp	val val glu val ile lys asp ser asn pro
3002	3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG	GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys	ala tyr ile gln ile thr tyr val glu pro
3062	3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA	ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg	ile thr tyr phe asp lys asn tyr asn leu
3122	3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT	TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr	leu asp gly arg ala his gly glu leu his
3182	3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT	ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr	thr ser his ala phe pro tyr ile lys thr
	ref 11.1
3242	3272
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC	ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile	ile leu thr pro ile glu val ala ile glu
3302	3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA	TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala	phe ala thr his gln asp pro ala asp pro
3362	3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT	GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser	val gly thr thr val asn gln gly pro leu
3422	3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA	CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile	pro ser asp pro lys leu phe arg his his
3482	3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT	ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe	thr lys arg cys glu asp ala leu arg lys

FIG. 4A (4 of 14)

3542	3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG	GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys	glu tyr gln arg glu leu gly lys leu ser
3602	3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT	CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro OCH	
3662	3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT	TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC
3722	3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC	TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG
3782	3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA	TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG
3842	3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA	GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG
3902	3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT	CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA
3962	3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA	GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT
4022	4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT	AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG
4082	4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA	TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC
4142	
CTC	

↓  
ref 12.1

FIG. 4A (5 of 14)

Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 341-360 of the cDNA. Exon sequence is underlined and represents nucleotides 365-381.

TTTTTTGAATTAATGGTGAGCAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTG  
AACAATTTTATGCTAGCTCATTGTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC  
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT  
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC  
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTG  
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATAACCAAAGATGG  
AAAGAGCTTTATAGATAACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG  
CCAGTTACAATCAATAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA  
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATC ACTTGAGATCAGGAGTTTGAGAC  
CCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAATTTTTTTTTTAAAT  
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT  
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG  
TTNTGATTTCNACACNTGCAACTCCCGCATTGGGTNAACAAAANCCAAGGAANC.

Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 341-360 of the cDNA. Exon sequence is underlined and represents nucleotides 372-381.

AATTAATGGTGAGCAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTGAACAAT  
TTTATGCTAGCTCATTGTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT  
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA  
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTCTCAGG  
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTGCTAGT  
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATAACCAAAGATGGAAAGA  
GCTTTATAGATAACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT  
NCAATCAATAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC  
AGCACTTTATAAGGCCCNAGGCNGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG  
CCTGGGCAACATANCAAGAGCCCATATCTACCAAAAAANTTTTTTTTTTAAATTAAG  
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCCNATNTNCCTTTGGAAAAGCTTANG  
AAGGGGAGGGCTTNCTTTGGANCCCCAAAAAGTTNAAAGGGNTTGCAGTCAGCCTTTT  
NAATCACCCNNGGNCCTNTTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT  
CNTNTTTTAAAAAANTNTTTTAAAGNANNTTTNTTNGN

Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 387-406 of the cDNA. Exon sequence is underlined and represents nucleotides 382-386.

TCTTNNGAAAAAGATTANATTATTAATTCTATGATATATTAACAATACACANCTCTAA  
CACTTGGAATTTTTTAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC  
TTCTCAAATATTTTTTAAAGTTCCTACAATGTTTTGTATTTGCTTAAAATAAAATANA  
AAAACCACCATATTACTTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT  
GTGTATGTCAACAAAAAAATTCACCTTAAATTTTTTTTTTCCATAAAAAACAGGGC  
TACTTGCCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA  
NTGTCGGNCCCTNCGTTTAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT  
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN  
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT  
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCINNACTNTTNN  
NCNCCCATCTTTNCNNTTNNNNNCCCCNTTTNNAATNNTTTNNNTNNCINNNTNATNT  
NTNAANNNACCNC

Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 387-406 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequence matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA  
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT  
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA  
AAACCCCATATTACTTTTCAGAAAANTATGCTAGCTAACAAATAGGACANAAAAATTCTG  
TGTATGCAACAAAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAACAGGG  
CTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG  
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG  
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGCT  
AAGCGTTCTTGCCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAA  
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA  
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC  
CGAATGGNATCTATTCCGGGAGACANATTACTATNGGATGANAGCANATNGCCCNAT  
GCTTNTTTGTAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNNT  
NNGCGANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNTGANTGNCT  
GGGAGAACCTACNTNCCCCNTACNNAATANNCTNACCCCCCTACTACTNTNNCNNTCNC  
TCTCTANTTCTACTCCACNTTATTATCCTCNNCCTTCNCATCNTCCCATCNTNATTCNAC  
GCCNCNANACTTANCNTTNATNCACTCTNNCT

Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-736.

TAATGTACATAGTGCTCATGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACA  
CCAGAACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA  
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA  
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCA  
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAATAATTTTAAACTATCAGGTTTACT  
GTATAACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAA  
TATTTCTACTTCTCATAAAACAGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC  
TTCTTTCTTAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCTGTATTTAT  
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA  
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA  
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAGGTTT  
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGGG  
TGAGGTGCCCCATGCCTT

Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-731.

TAACATAGTGCTCTGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACACCAGA  
ACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT  
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA  
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC  
ACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACTGTATA  
AACATATTTGACTAACCTAAAAGCCACATTCTTGATTTCCAATATAGCATCAATATTT  
CTACTTCTCATAAAACAGGGAAAACGTATNTACCAAAAATAACTTCTTATTACTTCCT  
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT  
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGGAGACATACTATTAAACCT  
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA  
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA  
TAAAGGTTTTNNGGGGAAAAGGGAAAAAATNGATTNCATNTCGNGGTTNGCAAGGTN  
TTTTCCATTGNGGGGNGGAGGGGCCCATGCCATAANTTTTAACCTTTCTTTTTTNGAAG  
AAATTAAACNNTTAAAGGGGTN

Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 925-945 of the cDNA. Exon sequence is underlined and represents nucleotides 813-920.

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC  
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGCAAGCTCTCAGCA  
GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA  
CTTTAGCTTTGGGCAGGAACCTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA  
AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCTTATCTTAGCCTTTATCCCCTTGT  
GGAAAAGACACTATCAATGCTAGATNCTCCAAGNCAGAGAATTATGCAGGTTTGGTC  
AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT  
TTTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNNGGTCTAGGACAT  
AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTTNG  
ANANGAATNNNCTGNGAAGGGCCCGATACGANAATTTGACTTCGGNGAAAATTNNNG  
GATTNNTACAAANTTCTAGGNGGCACCTTNAANAANGNNTGGGNACNTTGGNGGCGGA  
AAAAAGCCCTTCNTTTAGNTNTCCNGAAATGGAAAAGTNCCAANTTCCNAAAAAA  
ANGGGCTTTGTTNNCTTNCNANA

Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 929-949 of the cDNA. Exon sequence is underlined and represents nucleotides 813-924.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGGAAGGCCGATATCAACTATT  
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT  
ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA  
TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACCTTGTGGATGNTTATAA  
GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTTTTCC  
TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG  
NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT  
GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC  
TATNGANTATGNGGTTCTAGGACATGATTACATTTTTTNGGGAACTTCCATAGAATAAA  
CNTNTACCTNAAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAGTNC  
CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGGNCTTTAGNACGT  
TNGATNTTTGANCGGAAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC  
NAANAAGGNCTGTGTTNTTNGACATTTACCNGNNCCTTTCTAATCAAACNTNCTCTTC  
TNNNANCCNCANNCNNCCTATANNCTATCNCTCNNCTNNNCTCNTCACTCTCNC  
NCTNTCTTCCNTTCTNCACTNTNNNNTCNCTNNNATNNNCTTCTCCNATCCNTCTCANN  
NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCCT

Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1128-1147 of the cDNA. Exon sequence is underlined and represents nucleotides 1182-1270.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAACAAG  
GCCTGGCAGTTTCCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTTTTTTTC  
TNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTATCAGCTGA  
TGCAAAAGTGCTCAGTTTTATTTATGAAAATATTAAAGTTCCAGAAATATTAAGTGTCTTC  
TCCCAAACAGTTTTTAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGCCCCGTATTCTGC  
ATTCAGAATTTGGAAAATTGCCTCATTATAGATAGCCATNTCTTTTTTTTNTTTTTTTTAT  
NCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACATATGTATACATGTGC  
CATGTTGGTGTGCTGCACCCANNAACCCGCAATTTAACATTAGGTNTATCTCCAAATGCTA  
TCCNTTCACCTTCCCCCATNCCACAACAAGGCCCGGCGCNTTGNGATGTTCCCTTCCTG  
TGCCCACTGTGTNTCACATTNCCNCTTCCCNCCCTTANTNNNGTGCAGAACNTNGCCNGTN  
GCCCTNTNTTTTTTNNCCC

Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1128-1147 of the cDNA. Exon sequence is underlined and represents nucleotides 1152-1270.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGCAAT  
CGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCAACGGTA  
AAAACAATCCTCCTACAGAATTTTTTTTTTCTAGAAAGACAAATATTTACTAGGATATGCCC  
TTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTTATTTATGAAA  
ATATTAAAGTTCCAGAAATATTTAACTGTCTTCTCCCAACAGTTTTTAAAAAATGATACCTCA  
GGTTTATGGGGAAAAAAGCCCCGTATTCTGTCAATTCAGAAATTTGGAAAATTTGNCTCATT  
ATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTTTTTATACNTTTAAGTTTTTAAGGGGNAC  
CATGTTGCACCAANATTGCAGGGGTNGGTTACCATTATGGTTATTNCCATTGGTNCCCC  
CANTGTTTGGGGNGTTGGCTTTGCCACCCCCCAGNGTAAAACCNCCGNTGCGAATTTTTTA  
AAACAANTTTTGGGGGTATTANTNTTTCCCAAAAATNGGCNTTTTTNCCCTTTNCCCCC  
CTTTCNCCNCCCNNTTCCCAACNNANCAAGGGGCCCCCGGGTANTGGGGGAATAGNTTT  
CCCCCCTTNCCCTNGNNGGGCCAATTGTGGGGNNNCTCCATTTGGNNTGCAAANTTCCCC  
CACCCNTNATTGTTGGTGGNGAAACCATTTCCTGGGGGGTGGGGGGTTTTTTTTTGGTCCC  
CNTTGCCCAANTAATTTTTGCNTTGAANAAAAAGAATGGGGTTTTCCAAAGCTTTTNGTCN  
CCATTTGNTCCCTTTANGGNCCNTTNGTTCNCCTTNCCANAANGGGCCAATGTGAAACNN  
CCTTTCATTTTTTTTTTATTGGGGNTNCCNTTATGGN

Ref 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1514-1533 of the cDNA. Exon sequence is underlined and represents nucleotides 1536-1589.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTAC  
GTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTTCTTGTAGTTGTATATTGTA  
ATGATCATTGTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTTAAAAAGTGTTTAAAGTGT  
AACTGTGAATTAACTTGAATAATCATTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTA  
GGTGAGTCAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTT  
CTCTAGAAAGTCCTATCTAGAAAACCTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCC  
ATCCTCCCTTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGTTACAGCAAAAGTG  
AGCAAAGGTACAGAGATTTCCCATATAACCCCTTAGTATGCGTAGCCTCCCCCATTTAAC  
ATCCCCCATCAAGAGTAGTGCAATTTGTTGTAAGTGGTGAACCTACATTAACACATCATCAC  
CCAGAGTCCGCAGTTTACATTAGGGATCATTCATATAACATCTATTTTTTACTTTTTTTTTT  
TTAGTTGAGACAAGATTCTCGCTCTGTACCCAAGCTGGAGTGCAGTCCGNGTGGATTGTN  
GGCTTACTGNCN

Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1514-1533 of the cDNA. Exon sequence is underlined and represents nucleotides 1536-1589.

GTGCCGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTACGTACACAATAGCTT  
CTCCTCCTGGTGAGAATTTCTTCAATTTCTTGAGTTGTATATTGTAATGATCATTGTT  
GCTAGTCTTCAATGTCAATCCTATGCTTTTTTAAAAAGTGTTTTAAGTGTAAGTGNAAAT  
TAACTTGAATAATCATTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTAGGTGAGTC  
AGCATAACGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTAG  
AAAGTCCTCTCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATCC  
TCCCTTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTGA  
GCAAAGGGCAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTAAC  
ATCCCCATCAGAGTAAGNGCATTGTTGTAAGTGGNGAACCTACAATTNACACATTNTN  
ACCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCTANTAACACCTATTTTTT  
TTACTTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAAA  
CTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTGCN  
NTCNNCTTNNCNCNAAAGAANTTTTTTTTACCCTTTTTTTTTCCCCCNAANANANNAN  
CCTTCCCCTTGGNGGANGCTGGGGACTTCNCAGNGGNGG

Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1843-1861 of the cDNA. Exon sequence is underlined and represents nucleotides 1862-1918.

CAAAGTGCAGTTTATCTCAACACTGTTTTGCTCACAGAGAGCCTTGGTTTCAAAGGTAG  
GTTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGAT  
CATTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTA  
AAATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCC  
TTTTAGAATTTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTA  
ACTTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTT  
GTTTTCTCTTCACTTGGTTCTGTTTTTATAAAAAACTCAATTTATAAAGAATTCAATAT  
ATAAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTT  
GTTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATT  
CTTAAATTTTGAAGGTAGCTATTTCAATTTAATCATCCTAGAGGATGGAATGCANAGAT  
GTTGGATGAAAATAACTTACGTATTATTTTGTAAATAAATAAGAATTCATATATGGTT  
GATTACCTAAGTGGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNT  
NGATATATTATTT

Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1843-1861 of the cDNA. Exon sequence is underlined and represents nucleotides 1865-1918.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTCAAAGGTAGG  
TTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATC  
ATTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA  
AATTTAAATAATAACCTAAGACCCTTAATTCTTCTTTGCCTCTCTACTGCTGCCTGCC  
TTTAGAATTTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAA  
CTTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG  
NTTCTCTTCACTTGGTTCTGTTTTTATAAAAAACTCAATTTATAAAGAATTCAATATA  
TAAGCCATTCACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTG  
TTCACCTGCTTTAAATGNGACNTCNTAATATTTTGGNTTTCCTTAAGAAAATATGT  
ATAATCCTTAAANNTTNGAAAGGGANGCTANTTTCATTTTTTNAATCAATCCTAANAG  
GGATTGGGAAATGCNCAAGATTTTTTGTATTGAAAAANAACCTTANCGNATTTAATTTTT  
NGGNAATAAAATAATTAGNAATTCCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTA  
TTGCCCCATTTCNTTGATATGNAAAGCCTTTCACCAACCAATTTCCCNNTTGNNAGGAA  
TATTATTTTTTNANGGGCCTCNTNTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAAA  
GGGTCCCCNC

Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2413-2432 of the cDNA. Exon sequence is underlined and represents nucleotides 2433-2524.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAA  
TATCTTCCTGTGGGATGTGTAACATTTTCAGGTAGGAATCTTCCAGATGTACATTAAATC  
AAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTTAGTTTA  
TAAGGAAAGCTTAAAGACTTAAAGCCAATGCTTCACAAGGTGAATTAACATTTTCACAGTG  
ATTGTCATTAATACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTT  
ACCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCTTGNAATC  
CCGTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAA  
TTCTTAATTGGCTTTTACTTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATA  
AAATATTAAGATTATTTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAG  
TAGGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCT  
TGCTTTTTCTTCAAAACCTGTTAAATAGTAGGNTTGGGGATATTNTAAAAATTAGGTAA  
ATGGTATATCTTCTGGTGGAAANCAGAA

Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2413-2432 of the cDNA. Exon sequence is underlined and represents nucleotides 2445-2524.

CAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGTG  
GGATGTGTAACATTTTCAGGTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATCTT  
TTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTTAGTTTATAAGGAAAGCTT  
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTTCACAGTGATTGTCATTAAT  
ACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTACCTCTGAATTA  
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTT  
TAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCCTTAATTGGCT  
TNTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAATATTAGGAT  
TATTTTATGACTAATACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAA  
TTTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAAGTCANTTATGCCTTTGCTTTTT  
CTTCAAAACCCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAATTTCAAGC  
TNAAANTGGNTTATTATTCTNTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNAA  
NAAAAAGNTTATTCCNGGTTTCTTTNCGGNAAAAAAACCAAAAATCTTNGAAATTGTT  
TTTTACCAAAAANGACCTCCNCNGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACNN

Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2680-2699 of the cDNA. Exon sequence is underlined and represents nucleotides 2712-2800.

TTCCTATTCATGAAGCTAATCGGGATGCAAAGAACTATCCACAATTCATGGTAAACTT  
CAAGAAGCATTTCAGCAAAATTGTTTCATCAGGTAATGATTCCAATTTCTAGCTTCACTAT  
AAAGGGAAAAAACTGTCTGAAAGCATTAATGTTGTTTTGCACTGATGTCAAACCTAGATC  
CCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAATGATAGTTCATGGC  
CAAAGCAAAGCTCATTAACAATAAAAAATGAATTCACCTAAAGTAAATGGTGATCATCAT  
AAACTTTCTGCATAGCTTTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTTTA  
AAAATTGTGATTTTCTGTTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTTTAA  
AAATTGATACCCTATTNCTTTTGCTGNGGAAAANTGGAAGTTTTTTTAATATTTTCAAGG  
TTTTTTTTTAAAATTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAAACCTACCT  
AAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACCNTTTTATTTTTTTCCCCTAGGA  
ATGGTTTTACCCAAATCCATTCCCTTTTGAATAATATTTTTCCCTNAATTNCCCCAAAAA  
ANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGAAAATTAAAAAAATGGGGGTGGGGC  
CNTAAATGGGGATTATTTTTTAAATTTCTAAAAAAGGGANTTTTCCATTTACCTTTNAA  
TCCTTTTTGGGNGGNTTCNATTTATTGGGGAATCCTNCNCTTTTTTNTNCNCCTTAAAA  
AANTTAGGGCCTNCCAAAATTTTAAACCNTTTAATTTTTTNAAAANGGAAAGGGNCCCCT  
TTCTTNGCCCGGTTGGTTT

Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2909-2928 of the cDNA. Exon sequence is underlined and represents nucleotides 2929-2942.

TACAGATTGGAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT  
CTCTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA  
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT  
CTTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTCACACAT  
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA  
TAATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTAG  
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTTC  
CAGGTGAGGTTTCTTTAGAACGTAAAAGCCTGAAATCACACCTTAAAAACACTTCCTTT  
AACCTTTATAATTTCTTAATTTTACCATAAATGATTGCGTTTTATATTTACTGGGGCT  
AACTAGNATTTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTTGTTACTCAA  
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTCACCTGGGAGAATGGTTGGNAATGCAG  
AACCCTTAGACCCACCCCAGCCCCTGTGAAA

Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2909-29278 of the cDNA. Exon sequence is underlined and represents nucleotides 2931-2942.

CAGATAGTAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT  
CTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT  
AAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAATCT  
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTCACACATAT  
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA  
ATCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTTGAACTAGA  
ACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTTCC  
AGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTTTA  
ACCCTTTATAANTTNCTTAATTTTCACCCATAAAATNGATTGCNGTTTTATATTTTACC  
TNGGGNCTANACCTNAGGCAATTTTTCTGGGTCATAAGGGAAATTTCTTTTTCCCAAAC  
CCTTTTCTTCTTATTTTGTGTTGGGNCACCTCCCAAAGGTGNTCNGTTGGGGNTTNGGGN  
CCCCGNGAAAGGCCATTTGGGGGNTTCACCCCCGGGGGANGATTTGGTTTTGGAAAATN  
GTCNNNAAAACCTTCCNNACCCCCNNCCCCCNGGCCCCCNNTGNNNGGAAATCCAAAAGG  
ATCTTGNCNATTTTTTTTANCCAAANGANCNCCCCCNAGGGNGGGATTTTNGTTATTTCC  
CCAANAAGANGTAAGGTTNTTGGCCTTTNGGGGCNTTGGGTGTTTTNTTTNN

Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3377-3394 of the cDNA. Exon sequence is underlined and represents nucleotides 3268-3290.

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA  
TCGGTGTTAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAAC  
TATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAGATCAATNGTAA  
ACTTCATGTAACAATAAAATTCCAAACTTGGATTCTAAATGAANNAAAAANATCAACCT  
TTAAAGAAAAGCTGGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGACTCAA  
AATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCTGAGTGG  
TGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTTTAGGCA  
TGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCCTGCCGCT  
NAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNGNAAGNGNT  
CCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTCAGNGCTTCT  
TGCACCTCCTGNGCATCTCCCGTANTTCACCTCATTNACCNTNANTTTATAANNANN  
NAGCCACNTNNCCTATAGGCNATCNACGCNNTTCCCNNTANTCANTNNNAGACAATTT  
TTTNNCGCCCCCTCCTNNTCCTTCCTNNCTTCCNCCCNCCNCCCTNTNTCTNTNCCCC  
CNCCNNTTCTTANCTTNCT

Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3751-3770 of the cDNA. Exon sequence is underlined and represents nucleotides 3780-4119, and also represent the 3 terminus of the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATTG  
AAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGC  
TATGGTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTTAAGACATTTTAATGACTCAA  
AGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTATTCCT  
TTAAGTTCGTATTTTTTTAATTTATATTACCATTTATAGATTCATTTTGGAACCATTTTA  
AATGTAGTAATGCTTATTTTAAAGGTACTATTAAATATGTGAATGTTTACACTAATTTT  
ACCGAGTGGGACTTCAAAATTTTTTATTATTGACAATGGCTGAGAACAATTNAAGGGTTT  
GACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATTAAT  
GAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTTACATACCCAAAAACAGGAAATTT  
TAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATNTANT  
NTTAAATTTCCCGGGGGGANTAAATCTTAATNACCCCGGGTGGGGCCANNCNCCCCNTTA  
TAACTTTGGAATTTAAAAATTCNTTTTTNTNCAACCCCAAACCTGNANTNGGGTNNTTT  
TNAAGGAAAACCTTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCTNCNANAAANNG  
GGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCAAAAATTCCTTAATAAA  
ANCCCCGGGGCTCCCATTTNTAGNATTTTTTTTTTTGGCCCCACACTGTGTTNATTAAA  
NCCCCNCNTGCTAAAAATTTTTNNNGAAAANACCTNAACCCTTCTNNA

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 4B (1 of 5)

HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN	
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN	
rat	-----	
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN	
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK	
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSG--SVR---E	
HC5	-----	
	Cadherin	
	Cleavage	
HC2A	KLLRYSWFFFDVLIKSMAQHLENSKVKLIRNQRFPPASYHHAETVVNMLMPHITQKFGD	
KIAA	KLLKYSWFFFDVLIKSMAQHLENSKVKLIRNQRFPPASYHHAETVVNMLMPHITQKFRD	
rat	-----	
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPPKAYHHAHALHSLFLAIT-IVESQYAE	
HC1	HVLKHSWFFFAIILKSMAQHLEIDTNKIQLRPQRFPPESYQNELDNLMVLSDHVIWKYKD	
HC3	SALQQAWFFFELMVKSMVHHLYFNDKLEAPRKSRFPFERFMDIDIAALVSTIASDIVSRFQK	1.1/1.2/2.1/2.2
HC5	-----	
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDHKTLEFYKFEFL	
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLEFYKFEFL	
rat	-----	
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL	
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLKQYKFDL	
HC3	DEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVIIVSLRLDFL	3.1/3.2
HC5	-----	
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF	
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF	
rat	-----	
HC4	QTICNHEHYIPLNLPM-----AFAPKPKLQR-----VQDSNL---EYSLSDEY	
HC1	QEVQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF	
HC3	RIICSHEHYVTNLNPLCSLLTPPASPSVSSATISQSSGFSTNVQDQKIANMFELS--VPF	4.1/4.2
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSSQDQKIASMFDRTSRVPA	
	Cadherin	
	EC motif	
HC2A	CRNHFLVGLLLREVGTLQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
KIAA	CRNHFLVGLLLREVGTLQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
rat	-----	
HC4	CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ	
HC1	CRKHFLIGILLREVGTFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS	
HC3	RQQHYLAGLVLTETAVILDPDAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM	
HC5	SSTS-SPGLLFTETLAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA	
HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
rat	-----	
HC4	LYLPLFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS	
HC1	LYMPYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFS	
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS	
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT	

FIG. 4B (2 of 5)

		<u>Refs</u>
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS	
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKI PRPL	
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----	5.1/5.2
HC5	QNALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILPVCL	
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	
KIAA	HQFQYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNRSGVM	
HC1	QNFRLGKRNIIRKIAAAF--KFVQSTQNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK	
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGERGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS	
HC1	QHRSTLPIIRGK--NALSNPKL---LQMLDNTMTSNEIDIVHHVDTEANIATEGC	
HC3	RRSRGQIERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN	6.1/6.2
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVLSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFVC	
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLLKVLHSMACNQSAVYLQHCFAHQALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA	
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFPSAFFKGRVNMCAAFCEYVLKCCCTSKISTRNEASALLYLLMRNNFEYTKRKTFLRTH	
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH	
HC3	KFPPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK	7.1/7.2
HC5	KFGDLLFEEVEQCQFDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK	
HC2A	LQVIISVSQLIADVVGIGETRQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVIISVSQLIADVVGIGETRQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVIISLSQLIADVVGIGETRQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNANSRDLIPMLARAFPAEVKDLTKRIRTVLM	
HC1	LQIIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM	
HC3	MQVPMSLSLVLGTSQNFNEEFLRRSLKTLTYAEEDLELRETTFPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILY	

FIG. 4B (3 of 5)

	Transmembrane		
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV	
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV	
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV	
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKNGL	FSEAAMCYVHV	
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDL	LSEAAMCYIHI	
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTLWLQNMAGKHSERSN	HAEAAQCLVHS	
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLRLTLWLQNMAEKHTKKKQ	YTEAAMCLVHA	
	SH3		
HC2A	TALVAEYLTRKGV-----	-----FRQGCTAFRVITPN	
KIAA	TALVAEYLTRKEA-----	-----VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYLTRKEAD-----	-----LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFLHRKKL-----	-----FPNGCSAFKKITPN	
HC1	AALIAEYLKRKGYWKVEKICTASLLSEDTHPCDNSNLLTTPSGGSMFSGMWPAPLSITPN		
HC3	AALVAEYLSMLED-----	-----RKYLPVGCVTFOINISSN	8.1/8.2
HC5	AALVAEYLSMLED-----	-----HSYLPVGSVSFQINISSN	
	ITAM		
HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP	
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP	
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLELLEQCVNGLWKAERYEITISEISKLIGPI	
HC1	IKEEGAAKEDSGMHD-----	TPYNEINILVEQLYMCGEFLWKSERYELIADVKNKPIIAV	
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVLIP	
HC5	VLEESVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP		
	ITAM ITAM ITAM ITAM		
HC2A	YEKRRD-----	-----	
KIAA	YEKRRDFERLAHLTYDTLHRAYSKVT	TEVMHSGRRLGTIFRVAFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETTHLYDTLHRAYSKVT	EVITR-----A-----AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----	-----TFFRVAFYQG	
HC1	FEKQDFKLLSDLYDYDIHRSYLVKVAE	VNSEKRLFG-----RYRVAFYQG	
HC3	HEANRDAKKLSTIHGKLQEA	FSKIVHQSTGWERMFG-----TYFRVGFYG-	9.1
HC5	LEAHREFRKLTLTHSKLQRA	FDSIVNKH--KRMFG-----TYFRVGFYG-	
	ITAM ITAM		
HC2A	-FFEDGKEYIYKEPKLTPLSEISQRL	LLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDGKEYIYKEPKLTPLSEISQRL	LLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDGKEYIYKEPKLTPLSEISQRL	LLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA	
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRLV	KLYGEKFGTENVKIIQDSDKVNAKELDPKYA	
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRL	LLKLYADKFGADNVKIIQDSNKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEI	SHRLEAFYGERFGEDVVEVIKDSNPVDKCKLDPNKA	10.1/10.2
HC5	SKFGDLDEQEFVYKEPAITKLPEI	SHRLEAFYGCFFGAEFVEVIKDSTPVDKTKLDPNKA	
	ITAM		
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRRTILTA	
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRRTILTA	
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGV	EEQCKRRRTILTA	
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNISRFVFEAPYTL	SGKKQGCIEEQCKRRRTILT	
HC1	YIQVTVVTPFFEEKEIEDRKTD	FEMHNNIRFVFETPFTLSGKKHGGVAEQCKRRRTILT	
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAH	GELHEQFKRKTILT	
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRFRMYTTPFTLEGRPR	GELHEQYRRNTVLT	

FIG. 4B (4 of 5)



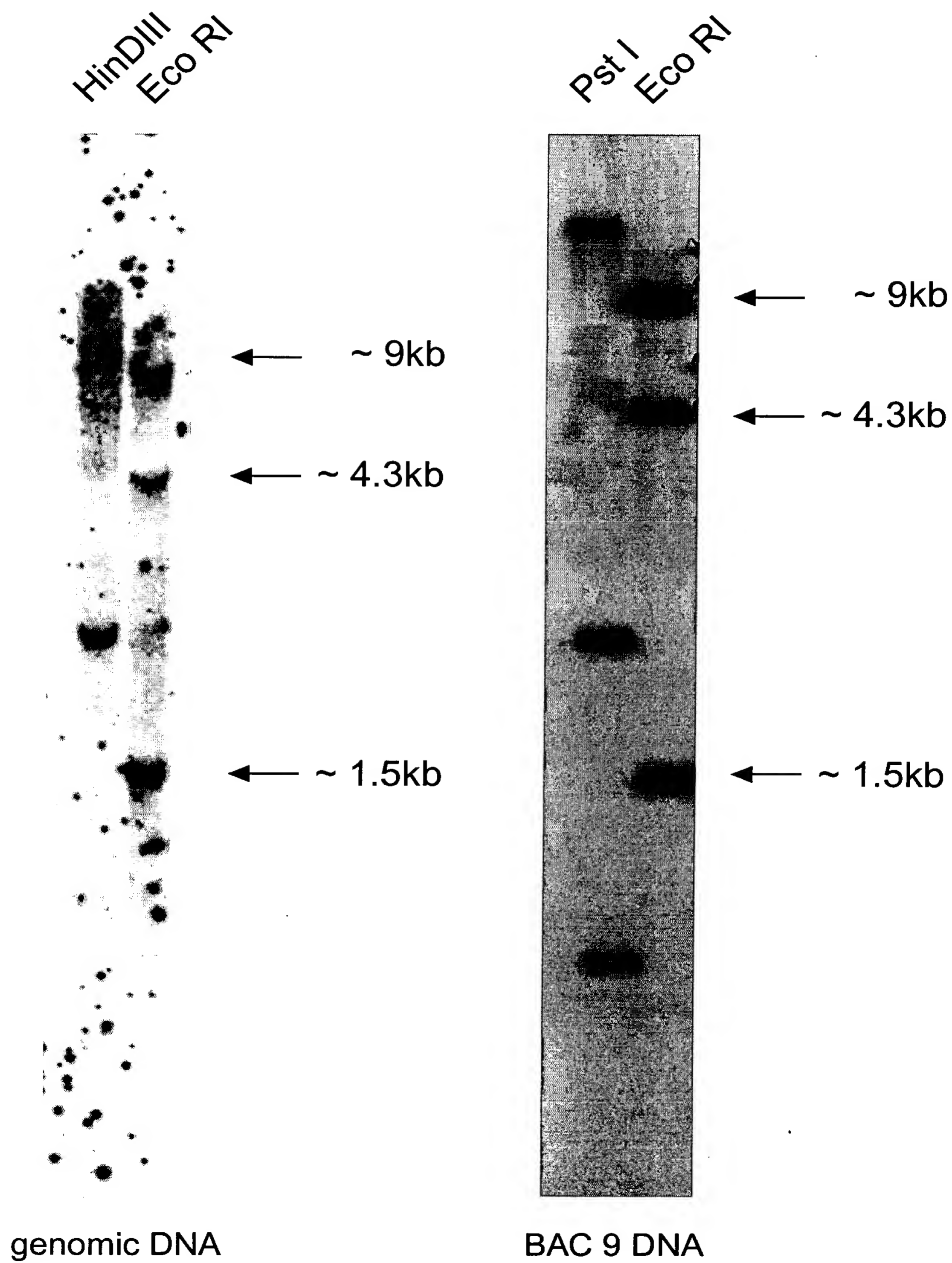


FIG. 5

-21

GTCGCCGTCGCCGCAGCAGCC -1

1/1	ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG	31/11	ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys		ile ser arg thr val ala ala glu val arg	
61/21	AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT	91/31	CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT
lys gln ile ser gly gln tyr ser gly ser		pro gln leu leu lys asn leu asn ile val	
121/41	GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC	151/51	CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG
gly asn ile ser his his thr thr val pro		leu thr glu ala val asp pro val asp leu	
181/61	GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT	211/71	GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT
glu asp tyr leu ile thr his pro leu ala		val asp ser gly pro leu arg asp leu ile	
241/81	GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	271/91	TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu phe pro pro asp asp ile glu val val		tyr ser pro arg asp cys arg thr leu val	
301/101	TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT	331/111	CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT
ser ala val pro glu glu ser glu met asp		pro his val arg asp cys ile arg ser tyr	
361/121	ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	391/131	TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC
thr glu asp trp ala ile val ile arg lys		tyr his lys leu gly thr gly phe asn pro	
421/141	AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	451/151	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
asn thr leu asp lys gln lys glu arg gln		lys gly leu pro lys gln val phe glu ser	
481/161	GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	511/171	GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA
asp glu ala pro asp gly asn ser tyr gln		asp asp gln asp asp leu lys arg arg ser	
541/181	ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC	571/191	TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT
met ser ile asp asp thr pro arg gly ser		trp ala cys ser ile phe asp leu lys asn	
601/201	TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA	631/211	CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC
ser leu pro asp ala leu leu pro asn leu		leu asp arg thr pro asn glu glu ile asp	
661/221	CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC	691/231	CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA
arg gln asn asp asp gln arg lys ser asn		arg his lys glu leu phe ala leu his pro	
721/241	TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG	751/251	CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
ser pro asp glu glu glu pro ile glu arg		leu ser val pro asp ile pro lys glu his	
781/261	TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA	811/271	TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC
phe gly gln arg leu leu val lys cys leu		ser leu lys phe glu ile glu ile glu pro	
841/281	ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC	871/291	AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT
ile phe ala ser leu ala leu tyr asp val		lys glu lys lys lys ile ser glu asn phe	
901/301	TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA	931/311	GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT
tyr phe asp leu asn ser glu gln met lys		gly leu leu arg pro his val pro pro ala	
961/321	GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT	991/331	TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT
ala ile thr thr leu ala arg ser ala ile		phe ser ile thr tyr pro ser gln asp val	

FIG. 6A (1 of 6)

1021/341	TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA	1051/351	CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
phe leu val ile lys leu glu lys val leu		gln gln gly asp ile gly glu cys ala glu	
1081/361	CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC	1111/371	ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
pro tyr met ile phe lys glu ala asp ala		thr lys asn lys glu lys leu glu lys leu	
1141/381	AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA	1171/391	CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
lys ser gln ala asp gln phe cys gln arg		leu gly lys tyr arg met pro phe ala trp	
1201/401	ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC	1231/411	AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
thr ala ile his leu met asn ile val ser		ser ala gly ser leu glu arg asp ser thr	
1261/421	GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA	1291/431	GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
glu val glu ile ser thr gly glu arg lys		gly ser trp ser glu arg arg asn ser ser	
1321/441	ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA	1351/451	ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
ile val gly arg arg ser leu glu arg thr		thr ser gly asp asp ala cys asn leu thr	
1381/461	AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA	1411/471	AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
ser phe arg pro ala thr leu thr val thr		asn phe phe lys gln glu gly asp arg leu	
1441/481	AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT	1471/491	GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
ser asp glu asp leu tyr lys phe leu ala		asp met arg arg pro ser ser val leu arg	
1501/501	CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG	1531/511	ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
arg leu arg pro ile thr ala gln leu lys		ile asp ile ser pro ala pro glu asn pro	
1561/521	CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA	1591/531	GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
his tyr cys leu thr pro glu leu leu gln		val lys leu tyr pro asp ser arg val arg	
1621/541	CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA	1651/551	AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
pro thr arg glu ile leu glu phe pro ala		arg asp val tyr val pro asn thr thr tyr	
1681/561	AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT	1711/571	CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
arg asn leu leu tyr ile tyr pro gln ser		leu asn phe ala asn arg gln gly ser ala	
1741/581	AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG	1771/591	TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
arg asn ile thr val lys val gln phe met		tyr gly glu asp pro ser asn ala met pro	
1801/601	GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA	1831/611	TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
val ile phe gly lys ser ser cys ser glu		phe ser lys glu ala tyr thr ala val val	
1861/621	TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA	1891/631	GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
tyr his asn arg ser pro asp phe his glu		glu ile lys val lys leu pro ala thr leu	
1921/641	ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT	1951/651	TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
thr asp his his his leu leu phe thr phe		tyr his val ser cys gln gln lys gln asn	
1981/661	ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA	2011/671	TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
thr pro leu glu thr pro val gly tyr thr		trp ile pro met leu gln asn gly arg leu	
2041/681	AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA	2071/691	TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
lys thr gly gln phe cys leu pro val ser		leu glu lys pro pro gln ala tyr ser val	
2101/701	CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG	2131/711	AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
leu ser pro glu val pro leu pro gly met		lys trp val asp asn his lys gly val phe	

FIG. 6A (2 of 6)

2161/721	2191/731
AAT GTT GAA GTT GTT GCT GTT TCG TCT ATC	CAT ACA CAA GAT CCT TAT CTT GAC AAA TTT
asn val glu val val ala val ser ser ile	his thr gln asp pro tyr leu asp lys phe
2221/741	2251/751
TTT GCT CTG GTC AAT GCT CTG GAT GAA CAC	CTG TTC CCA GTC CGA ATT GGG GAC ATG CGA
phe ala leu val asn ala leu asp glu his	leu phe pro val arg ile gly asp met arg
2281/761	2311/771
ATC ATG GAA AAT AAC TTA GAA AAT GAA TTG	AAG AGC AGT ATT TCA GCA CTG AAT TCA TCC
ile met glu asn asn leu glu asn glu leu	lys ser ser ile ser ala leu asn ser ser
2341/781	2371/791
CAG CTG GAA CCA GTG GTC CGA TTT CTT CAT	CTT CTG CTA GAT AAA CTG ATA CTT TTA GTT
gln leu glu pro val val arg phe leu his	leu leu leu asp lys leu ile leu leu val
2401/801	2431/811
ATT AGA CCT CCT GTC ATT GCT GGC CAA ATA	GTT AAC CTA GGT CAA GCA TCT TTT GAA GCC
ile arg pro pro val ile ala gly gln ile	val asn leu gly gln ala ser phe glu ala
2461/821	2491/831
ATG GCA TCA ATT ATA AAT CGA CTT CAC AAA	AAC TTG GAA GGA AAT CAT GAC CAG CAT GGC
met ala ser ile ile asn arg leu his lys	asn leu glu gly asn his asp gln his gly
2521/841	2551/851
AGA AAC AGC CTT CTT GCA TCA TAT ATT CAT	TAT GTT TTC CGC CTA CCA AAT ACT TAC CCT
arg asn ser leu leu ala ser tyr ile his	tyr val phe arg leu pro asn thr tyr pro
2581/861	2611/871
AAT TCA TCA TCA CCA GGT CCT GGG GGT TTG	GGA GGA TCA GTG CAT TAT GCC ACA ATG GCT
asn ser ser ser pro gly pro gly gly leu	gly gly ser val his tyr ala thr met ala
2641/881	2671/891
AGA TCT GCG GTG AGA CCT GCA AGC CTT AAT	TTA AAT CGT TCT CGA AGC CTT AGT AAT AGC
arg ser ala val arg pro ala ser leu asn	leu asn arg ser arg ser leu ser asn ser
2701/901	2731/911
AAT CCA GAT ATA TCT GGG ACT CCC ACG TCA	CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG
asn pro asp ile ser gly thr pro thr ser	pro asp asp glu val arg ser ile ile gly
2761/921	2791/931
AGT AAG GGT TTA GAT CGC TCC AAT TCC TGG	GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA
ser lys gly leu asp arg ser asn ser trp	val asn thr gly gly pro lys ala ala pro
2821/941	2851/951
TGG GGA TCC AAC CCC AGT CCA AGT GCA GAA	TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT
trp gly ser asn pro ser pro ser ala glu	ser thr gln ala met asp arg ser cys asn
2881/961	2911/971
CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT	TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA
arg met ser ser his thr glu thr ser ser	phe leu gln thr leu thr gly arg leu pro
2941/981	2971/991
ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT	TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT
thr lys lys leu phe his glu glu leu ala	leu gln trp val val cys ser gly ser val
3001/1001	3031/1011
CGG GAA TCA GCT TTG CAA CAA GCC TGG TTC	TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG
arg glu ser ala leu gln gln ala trp phe	phe phe glu leu met val lys ser met val
3061/1021	3091/1031
CAC CAT TTA TAC TTT AAT GAT AAA CTT GAG	GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT
his his leu tyr phe asn asp lys leu glu	ala pro arg lys ser arg phe pro glu arg
3121/1041	3151/1051
TTC ATG GAT GAC ATT GCA GCT CTT GTC AGC	ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT
phe met asp asp ile ala ala leu val ser	thr ile ala ser asp ile val ser arg phe
3181/1061	3211/1071
CAG AAG GAC ACA GAA ATG GTT GAG AGA CTC	AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT
gln lys asp thr glu met val glu arg leu	asn thr ser leu ala phe phe leu asn asp
3241/1081	3271/1091
CTG TTG TCT GTT ATG GAC AGA GGA TTT GTT	TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG
leu leu ser val met asp arg gly phe val	phe ser leu ile lys ser cys tyr lys gln

FIG. 6A (3 of 6)

3301/1101	GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT	3331/1111	CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
val ser ser lys leu tyr ser leu pro asn	3361/1121	pro ser val leu val ser leu arg leu asp	
TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC	3391/1131	TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA	
phe leu arg ile ile cys ser his glu his	3421/1141	tyr val thr leu asn leu pro cys ser leu	
CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT	3451/1151	GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA	
leu thr pro pro ala ser pro ser pro ser	3511/1171	val ser ser ala thr ser gln ser ser gly	
TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	3571/1191	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC	
phe ser thr asn val gln asp gln lys ile	3631/1211	ala asn met phe glu leu ser val pro phe	
CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	3691/1231	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT	
arg gln gln his tyr leu ala gly leu val	3751/1251	leu thr glu leu ala val ile leu asp pro	
GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	3811/1271	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC	
asp ala glu gly leu phe gly leu his lys	3871/1291	lys val ile asn met val his asn leu leu	
TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	3931/1311	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG	
ser ser his asp ser asp pro arg tyr ser	3991/1331	asp pro gln ile lys ala arg val ala met	
TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG	4051/1351	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA	
leu tyr leu pro leu ile gly ile ile met	4111/1371	glu thr val pro gln leu tyr asp phe thr	
GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT	4171/1391	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG	
glu thr his asn gln arg gly arg pro ile	4231/1411	cys ile ala thr asp asp tyr glu ser glu	
AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC	4291/1431	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA	
ser gly ser met ile ser gln thr val ala	4351/1451	met ala ile ala gly thr ser val pro gln	
CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	4411/1471	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT	
leu thr arg pro gly ser phe leu leu thr		ser thr ser gly arg gln his thr thr phe	
TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC		TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT	
ser ala glu ser ser arg ser leu leu ile		cys leu leu trp val leu lys asn ala asp	
GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT		CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA	
glu thr val leu gln lys trp phe thr asp		leu ser val leu gln leu asn arg leu leu	
GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT		GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA	
asp leu leu tyr leu cys val ser cys phe		glu tyr lys gly lys lys val phe glu arg	
ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA		GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT	
met asn ser leu thr phe lys lys ser lys		asp met arg ala lys leu glu glu ala ile	
CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG		GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA	
leu gly ser ile gly ala arg gln glu met		val arg arg ser arg gly gln leu glu arg	
AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA		GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT	
ser pro ser gly ser ala phe gly ser gln		glu asn leu arg trp arg lys asp met thr	
CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC		AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA	
his trp arg gln asn thr glu lys leu asp		lys ser arg ala glu ile glu his glu ala	
CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA		AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT	
leu ile asp gly asn leu ala thr glu ala		asn leu ile ile leu asp thr leu glu ile	

FIG. 6A (4 of 6)

4441/1481	GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC	4471/1491	AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
val val gln thr val ser val thr glu ser	lys glu ser ile leu gly gly val leu lys		
4501/1501	GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA	4531/1511	AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
val leu leu his ser met ala cys asn gln	ser ala val tyr leu gln his cys phe ala		
4561/1521	ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT	4591/1531	GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
thr gln arg ala leu val ser lys phe pro	glu leu leu phe glu glu glu thr glu gln		
4621/1541	TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA	4651/1551	CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
cys ala asp leu cys leu arg leu leu arg	his cys ser ser ser ile gly thr ile arg		
4681/1561	TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA	4711/1571	ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
ser his pro ser ala ser leu tyr leu leu	met arg gln asn phe glu ile gly asn asn		
4741/1581	TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG	4771/1591	TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
phe ala arg val lys met gln val pro met	ser leu ser ser leu val gly thr ser gln		
4801/1601	AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT	4831/1611	CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
asn phe asn glu glu phe leu arg arg ser	leu lys thr ile leu thr tyr ala glu glu		
4861/1621	GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT	4891/1631	GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
asp leu glu leu arg glu thr thr phe pro	asp gln val gln asp leu val phe asn leu		
4921/1641	CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG	4951/1651	AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
his met ile leu ser asp thr val lys met	lys glu his gln glu asp pro glu met leu		
4981/1661	ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT	5011/1671	TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
ile asp leu met tyr arg ile ala lys gly	tyr gln thr ser pro glu arg leu thr trp		
5041/1681	TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA	5071/1691	CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
leu gln asn met ala gly lys his ser glu	arg ser asn his ala glu ala ala gln cys		
5101/1701	CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA	5131/1711	TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
leu val his ser ala ala leu val ala glu	tyr leu ser met leu glu asp arg lys tyr		
5161/1721	CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT	5191/1731	ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
leu pro val gly cys val thr phe gln asn	ile ser ser asn val leu glu glu ser ala		
5221/1741	GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA	5251/1751	GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
val ser asp asp val val ser pro asp glu	glu gly ile cys ser gly lys tyr phe thr		
5281/1761	GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA	5311/1771	GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
glu ser gly leu val gly leu leu glu gln	ala ala ala ser phe ser met ala gly met		
5341/1781	TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA	5371/1791	CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
tyr glu ala val asn glu val tyr lys val	leu ile pro ile his glu ala asn arg asp		
5401/1801	GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA	5431/1811	CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
ala lys lys leu ser thr ile his gly lys	leu gln glu ala phe ser lys ile val his		
5461/1821	CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC	5491/1831	ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
gln ser thr gly trp glu arg met phe gly	thr tyr phe arg val gly phe tyr gly thr		
5521/1841	AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT	5551/1851	GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
lys phe gly asp leu asp glu gln glu phe	val tyr lys glu pro ala ile thr lys leu		

FIG. 6A (5 of 6)

5581/1861	5611/1871
GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT	TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
ala glu ile ser his arg leu glu gly phe	tyr gly glu arg phe gly glu asp val val
5641/1881	5671/1891
GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC	AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
glu val ile lys asp ser asn pro val asp	lys cys lys leu asp pro asn lys ala tyr
5701/1901	5731/1911
ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT	GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
ile gln ile thr tyr val glu pro tyr phe	asp thr tyr glu met lys asp arg ile thr
5761/1921	5791/1931
TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA	TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
tyr phe asp lys asn tyr asn leu arg arg	phe met tyr cys thr pro phe thr leu asp
5821/1941	5851/1951
GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA	TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
gly arg ala his gly glu leu his glu gln	phe lys arg lys thr ile leu thr thr ser
5881/1961	5911/1971
CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC	AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
his ala phe pro tyr ile lys thr arg val	asn val thr his lys glu glu ile ile leu
5941/1981	5971/1991
ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG	CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
thr pro ile glu val ala ile glu asp met	gln lys lys thr gln glu leu ala phe ala
6001/2001	6031/2011
ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG	CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
thr his gln asp pro ala asp pro lys met	leu gln met val leu gln gly ser val gly
6061/2021	6091/2031
ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT	GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
thr thr val asn gln gly pro leu glu val	ala gln val phe leu ser glu ile pro ser
6121/2041	6151/2051
GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA	CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
asp pro lys leu phe arg his his asn lys	leu arg leu cys phe lys asp phe thr lys
6181/2061	6211/2071
AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG	AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
arg cys glu asp ala leu arg lys asn lys	ser leu ile gly pro val gln lys glu tyr
6241/2081	6271/2091
CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA	
gln arg glu leu gly lys leu ser ser pro	OCH

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCTGCCCCTGCCACAGAGATTCC  
 TTCAGTCGAATGAGCTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTTCATCTGCAAAGAGCCATGTATTC  
 AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTTCATTGAAGAATGCAGTG  
 GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTTCGGGTAACAAGCTGTTA  
 TCTTTTAAGACATTTTAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT  
 TCACTTTAAGTTCGTATTTTTTAATTTATATCACCATTTATAGATTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA  
 TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGCGCGCCAGGGCCTC

FIG. 6A (6 of 6)

Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

Allelic Variations: Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

FIG. 6B

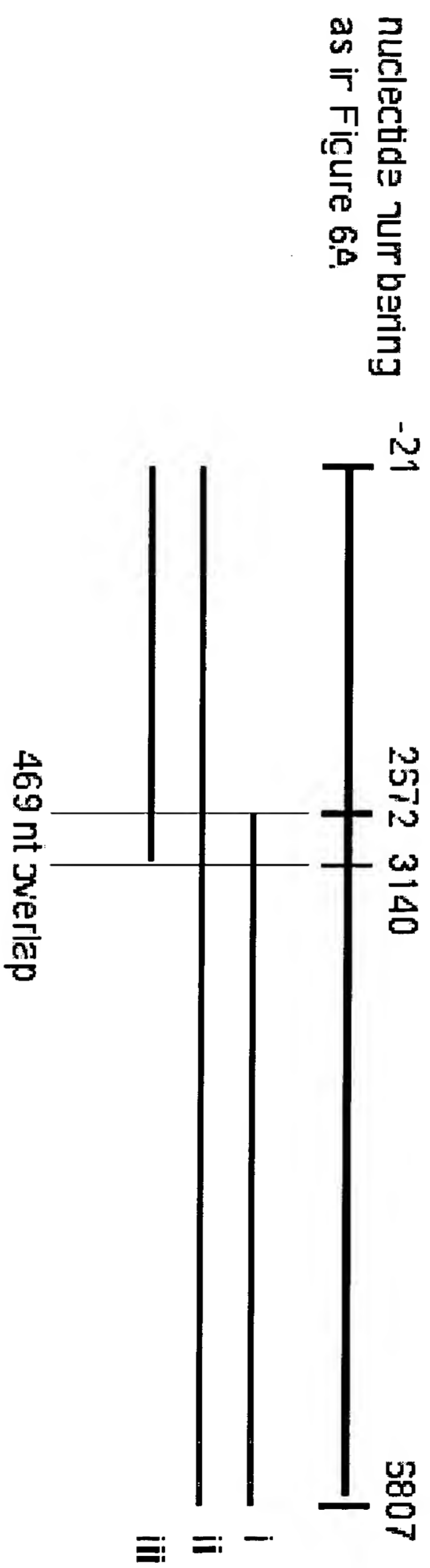


FIG. 6C

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGCCGCGCCTTCGCCCAGAAGATCAGCAGGT  
AAATATCCGGCGTGGGGCGC

Exon 85360 - 85510

GTTTTTGCTTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATCTCCGGACAATATAGTGGTTCTCCCAA  
CTGCTCAAAAACCTTAATATTGTTGGCAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 - 94720

TCTTATCCCAACTTTTTACAAAGGTGCCCCTTACCGAAGCAGTAGATCCAGTGGATTGGAAGATTACCTCATTACTCAT  
CCTTTGGCTGTGGATTCTGGGCCTTTACGGGATTTGATTGAATTCCTCCAGATGATATTGAAGTTGTTTATAGTCCTCG  
GGACTGCAGAACTCTTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACATTGACTTATT

Exon 94870 - 94980

TATTTTCCTTTTTTAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAGAAGTTATACAGAAGACTGGGCAATTGT  
CATCAGAAAGTAAGTTATATGTTTATTACAA

Exon 100110 - 100290

ATTTATTTAACTTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTTAATCCCAATACATTAGATAAACAGAAAG  
AAAGGCAAAAAGGTTTGCCAAAACAAGTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAAGTA  
ATACTTTTATTCTTAAATAA

Exon 100340 - 100600

ATATTTAATGTTTTGCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATAGATGATACCCCAAGGGGTAGCTGGGCC  
TGTAGTATCTTTGACTTGAAAAATTCACCTCCTGATGCTTTGCTTCCCAATTTACTTGATCGAACTCCAAATGAAGAAAT  
AGACCGTCAGAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACTTTTTGCTTTGCATCCATCACCAGATGAGGTAT  
AGATGTTTGCATATAAAGAA

Exon 100880-101020

TTTTGGTGTTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTTCTGATATACCCAAAGAACATTTTGGT  
CAAAGACTTCTTGTAATAATGCTTATCACTCAAGTGAGTATTTATTTCTTTTACTTACAAC

Exon 112010 – 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTGGCAAGTTTGGCTTTATATGATGTCAAGGAAAAGAAA  
AGGTAAGATTATATAATTTGACCATAGTTAT

Exon 113680 – 113880

AAGTTTAACATACTAATATTTTTTAGATTTTCAGAAAAC  
TTTTATTTTGACCTTAATTCTGAGCAGATGAAAGGGTTGT  
TA  
CGTCCACATGTACCACCTGCTGCCATTACTACCCTGGCAAGATCAGCAATTTTCTATCACTTATCCTTCCCAAGATGT  
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTTG

Exon 115020-115160

TTAATCTTAAC  
TTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGAGACATTGGAGAGTGTGCAGAACCATAT  
ATGATTTTCAAAGAAGCAGATGCCACCAAGGTAGAATGTTATGCTTCTCATTTCGCCAC

Exon 117200 – 117410

ATGTATAAAGTTCTGTTTTGCAGAATAAAGAAAAACTGGAGAACTGAAGAGTCAAGCAGATCAGTTTTGCCAAAGACTT  
GGGAAATATCGCATGCCTTTTGCTTGGA  
CTGCAATCCATTTAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAAGAGA  
TTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAAAC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTGTAGAACGAAAAGGGTCTTGGTCAGAGAGGAGGAATTCTAGTATTGTTGGCAG  
ACGATCACTTGAAAGGACAACAAGTGGAGATGATGCTTGTA  
ACTTGACGAGCTTTCGACCAGCTACTCTCACAGTGACAA  
ATTTTTTTAAGCAGGTATTGTTCTGTCATGTAGGAATTTT

(Next part of CLASP, starting  
GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACT  
AAGACCTATTACAG)

Exon 5560 — 5710

CTTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGAGAA  
GGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAGGTATTTAAAAATTTTGAGTAGAAATGGTTGCA

Exon 6680-6900

TTACATTGTTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTTCTCCCGCACCTGAAAATCCCCATTATTGC  
CTAACTCCGGAGCTGCTTCAAGTGAAGCTTTACCCTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCGC  
AAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTTGGAGAATTCTG

Exon 38920 — 39075

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACCCTCAGAGTCTTAATTTTGCCAATCGT  
CAAGGTTCTGCTAGAAATATAACAGTGAAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA



hCLASP4	-----MFPMEDISISVIGRQRRTVQ-----	20
hCLASP5	-----MTHLNSLDVQLAQELG-----	16
hCLASP3	-----MAERRAFAQKISRTVAAAEVRKQISGQYSGSPQLLKNLNIVG	41
hCLASP2	-----MLLFPYDDFQTAILRRQGRYICS-----	23
hCLASP7	-----MAASERRAFAHKINRTVAAAEVRKQVSRERSGSPHSSRRCSSSL	43
hCLASP1	MSFRGKVKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN	60
	... :	
hCLASP4	-----STVPEDA EKRAQSLFVKECIKTYSTDWHV VNYK	53
hCLASP5	-----DFT	19
hCLASP3	N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP	83
hCLASP2	-----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK	55
hCLASP7	G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP	79
hCLASP1	DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHV VNYK	120
	:	
hCLASP4	YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG	105
hCLASP5	DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI	63
hCLASP3	PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI	126
hCLASP2	YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG	107
hCLASP7	ADDLELLLQPRECR TTEP-GIPKD-EKLDAQVR-----AAVEMYIEDWVI	122
hCLASP1	YEQYSGDIRQLPRAEYKPEKLP SHSFEIDHEDADKDED TTS HSSSKGGGGAGGTGVFKSG	180
	: : . : * . : * .	
hCLASP4	WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDG SYILNSYKDEKNSKESK-GCIYLDACI	162
hCLASP5	VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPA AQA--GPRHLNVLC	118
hCLASP3	VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMSI	183
hCLASP2	WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDG SYNLNFYKDEKISKEPK-GSIFLDSCM	164
hCLASP7	VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVF EQDASGDERSGPEDSND SRRSGSGSP	179
hCLASP1	WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT	239
	: : : : * : : . : .	
hCLASP4	DVVQCPKMRRHAFELKMLDKYSHYLA AETE QEME EWLITLKKIIQINTDSL VQEKKETVE	222
hCLASP5	DVSGKG PVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARRTN-----RQAE	169
hCLASP3	DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQND DQRKSN-----RHKE	234
hCLASP2	GVVQNNKVRRFAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK	219
hCLASP7	EDTPRSSGASSI FDLRNLAADSL LPSLLERAAPEDVDRRNETLRRQH-----RPPA	230
hCLASP1	GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL	299
	* : * : : : :	
hCLASP4	TAQDDETSS----QGKAENIMASLERSMHP ELMKYGRETEQLNKLSRGDGRQNLFSFDSE	278
hCLASP5	LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE	212
hCLASP3	LFALHPSPD----EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE	277
hCLASP2	RNGDSHEDD----EQSKLEGSGGLDSYLP ELAKSAREAEIK---LKSES RVKLFYLDPD	272
hCLASP7	LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE	273
hCLASP1	TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTTRNMERLNLFSLDPD	359
	. : : : : : :	
hCLASP4	VQRLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGDNAKG PPTNVEPFFI	333
hCLASP5	IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARS AVFSV	268
hCLASP3	IEPIFAS----LALYDVKEKKKISENFYFDL NSEQMKGLLRPHVPPAAITTLARSAIFSI	333
hCLASP2	AQKLDFS----SAEPEVKS-FEEKFGKRI LVKCNDSL FN LQCCVAENEEGPTTNVEPFFV	327
hCLASP7	IEPIFGI----LALYDVREKKKISENFYFDL NSDSMKGLLRAHGTHPAISTLARSAIFSV	329
hCLASP1	IDTLKLQKDLLEPESVIKPFEEKAAKRIMI ICKALNSNLQGCVTENENDPITNIEPFFV	419
	: : : : : : : : * :	

FIG. 8 (1 of 6)



hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREKD-----MSQSPTS NFIRSCKNLLNVE	887
	.. *:: ** :.. ** : ..	:
hCLASP4	EIQVMIQFLPVILMQLFR-----VLTNMTH-----EDDVP	824
hCLASP5	RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFASFESVVAIANSLHNSKDLSKDQHG	775
hCLASP3	QLEPVVRFLHLLLDKLI LLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHQHG	840
hCLASP2	EGHVMIAFLPTILNQLFR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVVS LVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. : * : * : *	:
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVHYVFRLEPVQRDVPKSGAPTALLDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLSN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	:
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSY YCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKSN-----	972
	: . . .	:
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKH FHEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSTETSSFLQTLTGRLPTKKLFHEELALQWVVCSGSVRESALQQAWFF FELMVKSM	1019
hCLASP2	-----ADFLT SNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * .. : ***	:
	Cadherin Cleavage	
hCLASP4	ATYLLEENKIKLPRGQRFPEYHHVLSLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEFRRTFRSDRFMDDITTVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQKDTM---VERLNTISLAF	1076
hCLASP2	AQH LIENSKVKLLRNQRF PASYHHA AETV VNM LMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTPRKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQH LIDTNKIQLPRPQRFPESYQNELDNLMVLS DHVIWKYKDALEE---TRRATHSVAR	1052
	. : . : . * ** : . : : . . . . . * : *	:
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP----KVLAEYKFEFLQ TICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNLRHYCSQLSAKLSNL---PTLISMRL EFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVTNLNL	1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTNLNL	1059
hCLASP1	FLKRCFTFMDRGCVFKMVNNYISMFS S GDL----KTL CQYKFDFLQEV CQHEHFIP LCL	1107
	*: : : : * * : . . . . . * : : : * : : * : : * *	:

FIG. 8 (3 of 6)

Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSCSSFDQKIASMFDLTSEYRQQHFLTGLLFTELA	1085
hCLASP3	PCSLTTPPASPSVSSATSQSSGFSTNVQDQKIANMFELSVFPRQQHYLAGI	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFRCRNHFLVGLLLREVGT	1052
hCLASP7	PCCPLSPPASPSVSSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGI	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVG	1157
	. : : : : : * : : : *	
hCLASP4	ALQDN---YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLLENIQRL	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPKCVKPEVKVKIAALYLPLVGIILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNLSSHDSDPYSDPQIKARVAMLYLPLIGIIMETVP--	1254
hCLASP2	ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRI	1108
hCLASP7	ALEPEAEGAFLLHKKAISAVHSLLCGHDTDPYAEATVKARVAELYLPLLSIARDTLP--	1177
hCLASP1	ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPPLYGMLLDNMPRI	1213
	* : : : : : * * * : : : * * : : : *	
hCLASP4	AGRDTLYSCA-----AMPN-S---ASRDEFPCGFTSPANRGSLSLTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----	1162
hCLASP3	-----QLY-----DFTETHNQGRPICIAITDD--	1276
hCLASP2	NVRDVSPFPVNAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSRLASMLDSLTE	1201
hCLASP1	YKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSKDVLSIAAFSSIAIS	1273
	. :	
hCLASP4	FQ-NGHGIKREDSRGSLLIPEGATGFDPDQGNLTGEN-----TRQSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT	1208
hCLASP3	-----YESESGSMISQTVAMAIAGTSVPQLTR---PGSFLTSTSGRQHTTFSAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE	1327
	. : . : :	
hCLASP4	IRSLLMCYLYIVKMISEDTLTYWNKVSPQELINILILLEVCLFHFYRMYGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKQSSDKVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETVLQKWFTDLSVLQNLRLDLLYLVCVSCFEYKQKVFERNMNSL	1384
hCLASP2	IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEG	1287
hCLASP7	SRTLLACVLWVLKNTTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKQKKAFFERINSL	1309
hCLASP1	TRSLLMCFHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNFYLGKRNIIRKIAA	1387
	: . * : * : * . : : : : : : * : * * : :	
hCLASP4	WLSKHFGIDR-----KSQTMPALNRNRSGVMQARLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGEARGEMMRRAPGNDRFPGLNEN---	1311
hCLASP3	TFKKSMDRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLFVSRNRTGMMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSMDMKAR-----LEEAILGTIGARQEMVRRSRERSRPFGNPEN----	1350
hCLASP1	AFKFVQSTQNNGTCLKGSPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----	1442
	. : :	
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCCKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADVHLHQSLLLEANIATEVCLTALDTLSLFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTSRVDKTKDEMEHEALVEGNLATEASLVVLDLTLEIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTSNEIDIVHVDTEANIATEGCLTILDVSLFTQTHQRQLQ	1500
	. : : . . * * * * * * . .	

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hCLASP4	NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFCY	1419
hCLASP5	CKDS---LLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIAKFGDLLFEEVEQCFDLCH	1425
hCLASP3	SKES---ILGGVLKVLHSMACNQSAVYLQHC FATQRALVSKFPELLFEEETEQCADLCL	1546
hCLASP2	ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRADMCAALCY	1431
hCLASP7	ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL	1464
hCLASP1	QCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRL FVCKFPSAFFQGPADLCGSFCY	1560
	. : : : : ** * : : : * : : ** . : : : . : * : *	
hCLASP4	EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG	1479
hCLASP5	QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE	1483
hCLASP3	RLLRHCS SIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSSLSSLVGTSQNFNE	1604
hCLASP2	EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIISVSQLIADVVGIGE	1491
hCLASP7	RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGT TQNFSE	1522
hCLASP1	EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG	1619
	..*: * : . . . . **::** . : . : * : : : : : : . . . . *	
hCLASP4	SRFQESLFIINN FANS DRPMKATAFP AEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ	1539
hCLASP5	EHLRRSLR TILAYSEEDTAMQMPFPTQVEELL CNLNSILYDTVKMREFQEDPEMLMDLM	1543
hCLASP3	EFLRRSLKTILT YAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKEHQEDPEMLIDLQ	1664
hCLASP2	TRFQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ	1551
hCLASP7	EHLRRSLKTILT YAEEDMGLRDSTFAEQVQDLMFNLHMILTDTVMKEHQEDPEMLIDLQ	1582
hCLASP1	SRFQHSLAITNNFANGDKQMKN SNFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ	1679
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	transmembrane	
hCLASP4	YSLAKSYASTPELRKTWLD SMAKIHVKN GDFSEAMCYVHVAALVAEFLHRKK-----	1592
hCLASP5	YRIAKSYQASPDRLRLTWLQNM AEKHTKKKCYTEAAMCLVHAAALVAEYLSMLEDH-----	1598
hCLASP3	YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLED R-----	1718
hCLASP2	YSLAKSYASTPELRKTWLD SMARIHVKN GDLSEAMCYVHV TALVAEYLTRKG-----	1604
hCLASP7	YRIARGYQGS PDRLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLA LLEDQ-----	1637
hCLASP1	YSLANSYASTPELRRTWLESMAKIHARNGDLSEAMCYIHIAALIAEY LKRKG YWKVEKI	1739
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hCLASP4	-----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----	1622
hCLASP5	-----SYLPVGSVSFQNISSNVLEESV VSED TLSPDEDGV	1633
hCLASP3	-----KYLPGVCVTFQNISSNVLEESA VSDDVSPDEEGI	1753
hCLASP2	-----VFRQGCTAFRVITPNIDE EASMMEDVGMQD----	1634
hCLASP7	-----RHLPVGCVSFQNISSNVLEESA ISDDILSPDEEGF	1672
hCLASP1	CTASLLSEDT HPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGA AKEDSGMHD----	1795
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	ITAM	
hCLASP4	---VHYSEEV LLELLEQCVDGLWKAERYEIISEISK LIVPIY EKRRFEKLTQVYRTIHG	1679
hCLASP5	CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIP ILEAHREFRKLTLTHSKLQR	1693
hCLASP3	CSGKYFTESGLVGLLEQA AASF SMAGMYEAVNEVYKVLIP IHEANRDAKKLSTIHGKLQE	1813
hCLASP2	---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIPIY EKRR-----	1677
hCLASP7	CSGKHFTELGLVGLLEQA AGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKLQE	1732
hCLASP1	---TPYNENILVEQLYMCGEFLWK SERYELIADV NKPIIAVFEKQRDFKKLSDIYYDIHR	1852
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	ITAM DOCK motif DOCK motif ITAM	
hCLASP4	AYTKILEVMHTKKRL LGTFFRVAFY GQSF FEEEDGKEYIYKEPKLTGLSEISLRLV KLYG	1739
hCLASP5	AFDSIVNKDH--KRMFGTYFRVGF FG-SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYG	1750
hCLASP3	AFSKI VHQSTGWERMFGTYFRVGFYG-TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYG	1872
hCLASP2	-----DFFED EDGKEYIYKEPKLTPLSEISQRLLKLYS	1710
hCLASP7	AFTKIMHQSSGWERVFGTYFRVGFYG-AHFGDLDEQEFVYKEPSITKLAEISHRLEEFYT	1791
hCLASP1	SYLKVAEVVNSEKRLFG RYRVAFY GQGF FEEEEGKEYIYKEPKLTGLSEISQRLLKLYA	1912
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FIG. 8 (5 of 6)

	ITAM	ITAM	
hCLASP4	EKFGTENVKIIQDS	DKVNAKELDPKYAHIQV	TIYVKPYFDDKELTERKTEFERNHNISRFV 1799
hCLASP5	QCFGAEFVEVIKD	STPVDKTKLDPNKAYIQIT	TFVEPYFDEYEMKDRVITYFEKNFNLRRFM 1810
hCLASP3	ERFGEDVVEVIK	DSNPVDKCKLDPNKAYIQIT	TYVEPYFDTYEMKDRITYFDKNYNLRRFM 1932
hCLASP2	DKFGSENVKMIQ	DSGKVNPKDLDSKYAYIQV	THVIPFFDEKELQERKTEFERSHNIRRFM 1770
hCLASP7	ERFGDDVVEI	IKDSYPVDKSKLDSQKAYIQIT	TYVEPYFDTYELKDRVITYFDRNYGLRTFL 1851
hCLASP1	DKFGADNVKIIQ	DSNVNPKDLDPKYAYIQV	TIYVTPFFEEKEIEDRKTDFEMHHNINRFV 1972
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		ITAM	DOCK motif
hCLASP4	FEAPYTL	SGKKQGCIEEQCKRR	TILTTSNSFPYVKKRIPINCEQQINLKPIDGATDEIKD 1859
hCLASP5	YTPFTLE	GRPRGELHEQYRRNT	VLTTMHAFPIKTRISVIQKEEFVLTPIEVAIEDMCK 1870
hCLASP3	YCTPFTL	DGRAHGEHQFKRKT	ILTTSFAFPYIKTRVNVTHKEEIIILTPIEVAIEDMQK 1992
hCLASP2	FEMPFTQ	TGKRQGGVEEQCKRR	TILTAIHCFPIVKKRIPVMYQHHTDLNPIEVAIDEMSK 1830
hCLASP7	FCTPFTP	DGRAHGEHQHKKRKT	LLSTDHAFPIKTRIRVCHREETVLTPIEVAIEDMQK 1911
hCLASP1	FETPFTL	SGKKHGGVAEQCKRR	TILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSR 2032
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	Coiled-coil		
hCLASP4	KTAE	LQKLCSS	TDVDMIQLQLKLGWVSQVNAGPLAYARAF
hCLASP5	KTLL	QAVAINQEP	PDAMKLMVLQGSVGATVNQGP
hCLASP3	KTQEL	AFATHQDP	ADPKMLQMVLGSGVTTVNQGP
hCLASP2	KVAEL	RQLCSSAE	VDMIKLQLKLGSSVSQVNAGPLAYARAF
hCLASP7	KTREL	AFATEQDP	PDAMKLMVLQGSVGPTVNQGP
hCLASP1	KVSEL	NQLCTMEE	VDMISLQLKLGSSSVKVNAGPMAYARAF
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	Coiled-coil		
hCLASP4	DMFRKFIQACS	I	ALELNERLIKEDQVEYHEGLKSNFRDMVKELSDTIHEQILQEDTMHSP 1979
hCLASP5	LCFKEFIMRCGE	A	VEKNKRLITADQREYQQLKKNYNKLKENLRPMIERKIPELYKPIFR 1990
hCLASP3	LCFKDFTKRCED	A	LRKNKSLIGPVQKEYQRELGLSSP----- 2090
hCLASP2	EVFRQFVEACGO	A	LAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS- 1949
hCLASP7	LCFKDFCKKCED	A	LRKNKALIGPDQKEYHRELERNYCRLREALQPLLTQRLPQLMAPTP- 2030
hCLASP1	EI	FRQFADACGO	ALDVNERLIKEDQLEYQEELRSHYKDMLSELSTVMNEQITGRDDLSCR 2152
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	PDZ ligand		
hCLASP4	WMSNTLHV	FCAISGTSSDRGYGSPRYAEV	-- 2008
hCLASP5	VESQKRDS	FSHRSSFRKCETQLSQGS	----- 2015
hCLASP3	-----		
hCLASP2	VLPNSLHIF	NAISGTP	STMVHGMTSSSSVV 1980
hCLASP7	--PGLRNSL	NRASFRKADL	----- 2047
hCLASP1	GVDQTCT	RVISKATPALPTVSISSAEV	--- 2180

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